K. Lacourcière

```
                    RAW SEQUENCE LISTING           DATE: 11/27/2000
                    PATENT APPLICATION:  US/09/496,231A     TIME: 17:39:41

                    Input Set : A:\PTO.txt
                    Output Set: N:\CRF3\11272000\I496231A.raw

        4 <110> APPLICANT: Hubbell, Jeffrey A.
        5          Elbert, Donald
        6          Lutolf, Matthias
        7          Pratt, Alison
        8          Schoenmakers, Ronald
        9          Tirelli, Nicola
       10          Vernon, Brent
       12 <120> TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC
       13          ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS
       16 <130> FILE REFERENCE: 50154/002002
       18 <140> CURRENT APPLICATION NUMBER: 09/496,231A
       19 <141> CURRENT FILING DATE: 2000-02-01
       21 <150> PRIOR APPLICATION NUMBER: 60/118,093
       22 <151> PRIOR FILING DATE: 1999-02-01
       24 <160> NUMBER OF SEQ ID NOS: 74
       26 <170> SOFTWARE: FastSEQ for Windows Version 4.0


   ERRORED SEQUENCES

       28 <210> SEQ ID NO: 1
       29 <211> LENGTH: 10
       30 <212> TYPE: PRT
       31 <213> ORGANISM: Artificial Sequence
       33 <220> FEATURE:
       34 <223> OTHER INFORMATION: Based on Homo sapiens
       36 <221> NAME/KEY: VARIANT
       37 <222> LOCATION: (1)...(10)
       38 <223> OTHER INFORMATION: Xaa=any amino acid except Cys
       40 <400> SEQUENCE: 1
E-->   41 Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Tyr 1                    5                    10
       43 <210> SEQ ID NO: 2
       44 <211> LENGTH: 8
       45 <212> TYPE: PRT
       46 <213> ORGANISM: Artificial Sequence
       48 <220> FEATURE:
       49 <223> OTHER INFORMATION: Based on Homo sapiens
       51 <221> NAME/KEY: VARIANT
       52 <222> LOCATION: (1)...(8)
       53 <223> OTHER INFORMATION: Xaa=any amino acid except Cys
       55 <400> SEQUENCE: 2
E-->   56 Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys 1                    5
       58 <210> SEQ ID NO: 3
       59 <211> LENGTH: 6
       60 <212> TYPE: PRT
       61 <213> ORGANISM: Artificial Sequence
       63 <220> FEATURE:
```

Does Not Comply
Corrected Diskette Needed

insert hard return (handwritten annotation near line 41)

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        64 <223> OTHER INFORMATION: Based on Homo sapiens
        66 <221> NAME/KEY: VARIANT
        67 <222> LOCATION: (1)...(6)
        68 <223> OTHER INFORMATION: Xaa=any amino acid except Cys
        70 <400> SEQUENCE: 3
E--> 71 Xaa Xaa Xaa Xaa Xaa Xaa 1                    5
        73 <210> SEQ ID NO: 4
        74 <211> LENGTH: 13
        75 <212> TYPE: PRT
        76 <213> ORGANISM: Artificial Sequence
        78 <220> FEATURE:
        79 <223> OTHER INFORMATION: Based on Homo sapiens
        81 <221> NAME/KEY: VARIANT
        82 <222> LOCATION: (1)...(13)
        83 <223> OTHER INFORMATION: Xaa=any amino acid except Cys
        85 <400> SEQUENCE: 4
        86 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys 1          5
E--> 87 10
        89 <210> SEQ ID NO: 5
        90 <211> LENGTH: 7
        91 <212> TYPE: PRT
        92 <213> ORGANISM: Artificial Sequence
        94 <220> FEATURE:
        95 <223> OTHER INFORMATION: Based on Homo sapiens
        97 <221> NAME/KEY: VARIANT
        98 <222> LOCATION: (1)...(7)
        99 <223> OTHER INFORMATION: Xaa=any amino acid except Cys
       101 <400> SEQUENCE: 5
E--> 102 Cys Xaa Xaa Xaa Xaa Xaa Cys 1                5
       129 <210> SEQ ID NO: 7
       130 <211> LENGTH: 5
       131 <212> TYPE: PRT
       132 <213> ORGANISM: Artificial Sequence
       134 <220> FEATURE:
       135 <223> OTHER INFORMATION: Based on Homo sapiens
       137 <221> NAME/KEY: VARIANT
       138 <222> LOCATION: (1)...(5)
       139 <223> OTHER INFORMATION: Xaa=any amino acid except Cys or Tyr
       141 <400> SEQUENCE: 7
E--> 142 Xaa Xaa Xaa Xaa Xaa 1                    5
       144 <210> SEQ ID NO: 8
       145 <211> LENGTH: 6
       146 <212> TYPE: PRT
       147 <213> ORGANISM: Artificial Sequence
       149 <220> FEATURE:
       150 <223> OTHER INFORMATION: Based on Homo sapiens
       152 <400> SEQUENCE: 8
E--> 153 Gly Pro Arg Val Val Glu 1                5
       155 <210> SEQ ID NO: 9
```

```
       156 <211> LENGTH: 6
       157 <212> TYPE: PRT
       158 <213> ORGANISM: Artificial Sequence
       160 <220> FEATURE:
       161 <223> OTHER INFORMATION: Based on Homo sapiens
       163 <400> SEQUENCE: 9
E--> 164 Asn Asn Arg Asp Asn Thr 1              5
       166 <210> SEQ ID NO: 10
       167 <211> LENGTH: 6
       168 <212> TYPE: PRT
       169 <213> ORGANISM: Artificial Sequence
       171 <220> FEATURE:
       172 <223> OTHER INFORMATION: Based on Homo sapiens
       174 <400> SEQUENCE: 10
E--> 175 Tyr Asn Arg Val Ser Glu 1              5
       177 <210> SEQ ID NO: 11
       178 <211> LENGTH: 6
       179 <212> TYPE: PRT
       180 <213> ORGANISM: Artificial Sequence
       182 <220> FEATURE:
       183 <223> OTHER INFORMATION: Based on Homo sapiens
       185 <400> SEQUENCE: 11
E--> 186 Gln Met Arg Met Glu Leu 1              5
       188 <210> SEQ ID NO: 12
       189 <211> LENGTH: 6
       190 <212> TYPE: PRT
       191 <213> ORGANISM: Artificial Sequence
       193 <220> FEATURE:
       194 <223> OTHER INFORMATION: Based on Homo sapiens
       196 <400> SEQUENCE: 12
E--> 197 Gly Phe Arg His Arg His 1              5
       199 <210> SEQ ID NO: 13
       200 <211> LENGTH: 6
       201 <212> TYPE: PRT
       202 <213> ORGANISM: Artificial Sequence
       204 <220> FEATURE:
       205 <223> OTHER INFORMATION: Based on Homo sapiens
       207 <400> SEQUENCE: 13
E--> 208 Gly Tyr Arg Ala Arg Pro 1              5
       210 <210> SEQ ID NO: 14
       211 <211> LENGTH: 6
       212 <212> TYPE: PRT
       213 <213> ORGANISM: Artificial Sequence
       215 <220> FEATURE:
       216 <223> OTHER INFORMATION: Based on Homo sapiens
       218 <400> SEQUENCE: 14
E--> 219 Tyr Gln Lys Asn Asn Lys 1              5
       221 <210> SEQ ID NO: 15
       222 <211> LENGTH: 6
```

```
        223 <212> TYPE: PRT
        224 <213> ORGANISM: Artificial Sequence
        226 <220> FEATURE:
        227 <223> OTHER INFORMATION: Based on Homo sapiens
        229 <400> SEQUENCE: 15
E--> 230 Leu Ile Lys Met Lys Pro 1               5
        232 <210> SEQ ID NO: 16
        233 <211> LENGTH: 6
        234 <212> TYPE: PRT
        235 <213> ORGANISM: Artificial Sequence
        237 <220> FEATURE:
        238 <223> OTHER INFORMATION: Based on Homo sapiens
        240 <400> SEQUENCE: 16
E--> 241 Asn Phe Lys Ser Gln Leu 1               5
        243 <210> SEQ ID NO: 17
        244 <211> LENGTH: 6
        245 <212> TYPE: PRT
        246 <213> ORGANISM: Artificial Sequence
        248 <220> FEATURE:
        249 <223> OTHER INFORMATION: Based on Homo sapiens
        251 <400> SEQUENCE: 17
E--> 252 Glu Trp Lys Ala Leu Thr 1               5
        254 <210> SEQ ID NO: 18
        255 <211> LENGTH: 6
        256 <212> TYPE: PRT
        257 <213> ORGANISM: Artificial Sequence
        259 <220> FEATURE:
        260 <223> OTHER INFORMATION: Based on Homo sapiens
        262 <400> SEQUENCE: 18
E--> 263 Ser Tyr Lys Met Ala Asp 1               5
        265 <210> SEQ ID NO: 19
        266 <211> LENGTH: 6
        267 <212> TYPE: PRT
        268 <213> ORGANISM: Artificial Sequence
        270 <220> FEATURE:
        271 <223> OTHER INFORMATION: Based on Homo sapiens
        273 <400> SEQUENCE: 19
E--> 274 Thr Gln Lys Lys Val Glu 1               5
        276 <210> SEQ ID NO: 20
        277 <211> LENGTH: 6
        278 <212> TYPE: PRT
        279 <213> ORGANISM: Artificial Sequence
        281 <220> FEATURE:
        282 <223> OTHER INFORMATION: Based on Homo sapiens
        284 <400> SEQUENCE: 20
E--> 285 Arg Gln Lys Gln Val Lys 1               5
        300 <210> SEQ ID NO: 22
        301 <211> LENGTH: 6
        302 <212> TYPE: PRT
```

```
       303 <213> ORGANISM: Artificial Sequence
       305 <220> FEATURE:
       306 <223> OTHER INFORMATION: Based on Homo sapiens
       308 <400> SEQUENCE: 22
E--> 309 Leu Ile Lys Ala Ile Gln 1                    5
       640 <210> SEQ ID NO: 53
       641 <211> LENGTH: 28
       642 <212> TYPE: PRT
       643 <213> ORGANISM: Artificial Sequence
       645 <220> FEATURE:
       646 <223> OTHER INFORMATION: Based on Homo sapiens
       648 <400> SEQUENCE: 53
       649 Arg Pro Ser Leu Ala Lys Lys Gln Arg Phe Arg His Arg Asn Arg Lys 1
E--> 650 5                10              15       Gly Tyr Arg Ser Gln Arg Gly His
E--> 651 Ser Arg Gly Arg               20                25
       840 <210> SEQ ID NO: 69
       841 <211> LENGTH: 156
       842 <212> TYPE: PRT
       843 <213> ORGANISM: Artificial Sequence
       845 <220> FEATURE:
       846 <223> OTHER INFORMATION: Based on Homo sapiens
       848 <400> SEQUENCE: 69
       849 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro 1
E--> 850 5                10              15       Arg Gly Ser His Met Lys Asp Pro
       851 Lys Arg Leu Tyr Arg Ser Arg Lys         20                25
E--> 852 30          Leu Pro Val Glu Leu Glu Ser Ser His Pro Ile Phe His Arg Gly
E--> 853 35              40                  45          Glu Phe Ser Val Cys Asp
       854 Ser Val Ser Val Trp Val Gly Asp Lys Thr    50                55
E--> 855 60                  Thr Ala Thr Asp Ile Lys Gly Lys Glu Val Met Val Leu Gly Glu
E--> 856 Val65               70                  75                80    Asn Ile Asn
       857 Asn Ser Val Phe Lys Gln Tyr Phe Phe Glu Thr Lys Cys           85
E--> 858 90              95      Arg Asp Pro Asn Pro Val Asp Ser Gly Cys Arg Gly Ile
E--> 859 Asp Ser Lys         100             105             110         His
       860 Trp Asn Ser Tyr Cys Thr Thr Thr His Thr Phe Val Lys Ala Leu       115
E--> 861 120             125             Thr Met Asp Gly Lys Gln Ala Ala Trp Arg Phe
       862 Ile Arg Ile Asp Thr    130             135             140
       863 Ala Cys Val Cys Val Leu Ser Arg Lys Ala Val Arg145           150
E--> 864 155
       866 <210> SEQ ID NO: 70
       867 <211> LENGTH: 429
       868 <212> TYPE: DNA
       869 <213> ORGANISM: Artificial Sequence
       871 <220> FEATURE:
       872 <223> OTHER INFORMATION: Based on Homo sapiens
       874 <400> SEQUENCE: 70
E--> 875 gaattcccat ggcatatgaa gacccgaaac gtctgtaccg ttctcgtaaa ctgcccgtgg  60
W--> 876 60aactcgagag ctcctcccac ccgattttcc atcgtggcga gttctccgtg tgtgactctg
W--> 877 120tctgtatggg taggcgataa aaccactgcc actgatatca aaggcaaaga ggtgatggtg
W--> 878 180ctgggagaag taaacattaa caactctgta ttcaaacagt acttcttcga aactaagtgc
```

```
W--> 879 240cgtgacccga acccggtaga ctctgggtgt cgcggcatcg attctaaaca ctggaactct
W--> 880 300tactgcacca ctactcacac tttcgttaaa gcgttgacta tggatggtaa acaggctgcc
W--> 881 360tggcgtttca tccgtatcga tactgcatgc gtgtgtgtac tgtcccgtaa agctgttcgt
E--> 882 420taaggatcc                                                      429
```

VERIFICATION SUMMARY   DATE: 11/27/2000
PATENT APPLICATION: US/09/496,231A   TIME: 17:39:42

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I496231A.raw

```
L:41 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:1
L:56 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:2
L:71 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:3
L:87 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:87 M:252 E: No. of Seq. differs, <211>LENGTH:Input:13 Found:0 SEQ:4
L:102 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:0 SEQ:5
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:0 SEQ:7
L:153 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:8
L:164 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:9
L:175 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:10
L:186 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:11
L:197 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:12
L:208 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:13
L:219 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:14
L:230 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:15
L:241 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:16
L:252 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:17
L:263 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:18
L:274 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:19
L:285 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:20
L:309 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:22
L:320 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:23
L:331 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:24
L:343 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:25
L:351 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:26
L:359 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:27
L:370 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:28
L:378 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:29
L:386 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:30
L:394 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:31
L:405 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:32
L:416 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:33
L:427 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:34
L:438 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:35
L:449 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:36
L:460 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:37
L:471 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:38
L:482 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:39
L:493 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:40
L:504 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:41
L:515 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:0 SEQ:42
L:526 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:0 SEQ:43
L:537 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:0 SEQ:44
L:548 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:0 SEQ:45
L:559 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:46
L:570 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:47
L:581 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:48
```

VERIFICATION SUMMARY   DATE: 11/27/2000
PATENT APPLICATION: US/09/496,231A   TIME: 17:39:42

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I496231A.raw

```
L:596 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:49
L:615 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:50
L:626 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:51
L:638 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:638 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:3 SEQ:52
L:650 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:663 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:692 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:56
L:726 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:59
L:738 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:60
L:750 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:779 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:63
L:802 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:65
L:827 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:67
L:850 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:852 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:69
L:852 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=69
L:853 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:855 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:856 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:856 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:858 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:875 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:70
L:876 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:877 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:877 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:878 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:879 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:880 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:880 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:881 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
M:254 Repeated in SeqNo=70
L:882 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
```